



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure



BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

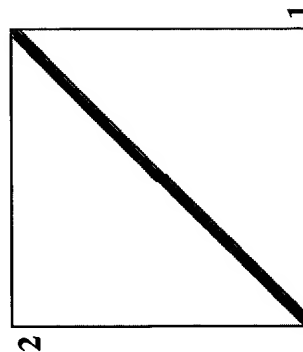
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation

Sequence 1: lcl|SEQID NO:2

Length = 300 (1 .. 300)

Sequence 2: gi|4507585|ref|NP_003814.1|tumor necrosis factor receptor superfamily, member 6b [Homo sapiens]

Length = 300 (1 .. 300)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 634 bits (1634), Expect = 3e-180
Identities = 300/300 (100%), Positives = 300/300 (100%), Gaps = 0/300 (0%)

Blast Result

Query	1	MRALEGPGLSLLCVLALPALLPVP	PAVRGVAETPTY	PWRDAETGERLV	CAQCPPGTFVQR	60
Sbjct	1	MRALEGPGLSLLCVLALPALLPVP	PAVRGVAETPTY	PWRDAETGERLV	CAQCPPGTFVQR	60
Query	61	PCRRDSP TTCGPPRHYTQFWNYL	ERCYCNVLCGEREEEE	ARACHATHNRAC	RCRTGFF	120
Sbjct	61	PCRRDSP TTCGPPRHYTQFWNYL	ERCYCNVLCGEREEEE	ARACHATHNRAC	RCRTGFF	120
Query	121	AHAGFCLEHASCPPPGAGVIAPG	TPSQNTQCQPCPPGTF	SASSSSSEQCQPHR	NCTALGLA	180
Sbjct	121	AHAGFCLEHASCPPPGAGVIAPG	TPSQNTQCQPCPPGTF	SASSSSSEQCQPHR	NCTALGLA	180
Query	181	LNVPGSSSHDTLCTSGTFPLSTR	VPGAEECERAVIDF	VAFQDISIKRLQ	RLLQALEAPE	240
Sbjct	181	LNVPGSSSHDTLCTSGTFPLSTR	VPGAEECERAVIDF	VAFQDISIKRLQ	RLLQALEAPE	240
Query	241	GWGPTPRAGRAALQLKLRRL	TELLGAQDGA	LIVRLQLALRV	ARMPLERSVRERFLPVH	300
Sbjct	241	GWGPTPRAGRAALQLKLRRL	TELLGAQDGA	LIVRLQLALRV	ARMPLERSVRERFLPVH	300

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H 0.323 0.137 0.454

Gapped Lambda K H 0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 1174
Number of extensions: 513
Number of successful extensions: 7
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 300
Length of database: 1,238,234,516

Length adjustment: 132
Effective length of query: 168
Effective length of database: 1,238,234,384
Effective search space: 208023376512
Effective search space used: 208023376512
Neighboring words threshold: 9
X1: 16 (7.5 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (22.0 bits)
S2: 78 (34.7 bits)